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10/565,278	06/30/2006	Sheila Marie Schmutz	046423-0006US	7966
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary

Application No.

10/565,278

Applicant(s)

SCHMUTZ ET AL.

Examiner

KATHERINE SALMON

Art Unit

1634

Period for Reply -- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 09 September 2008.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-19 is/are pending in the application.
- 4a) Of the above claim(s) 10 and 12-15 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-9, 11 and 16-19 is/are rejected.
- 7) ☒ Claim(s) 1-9, 11 and 16-19 is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
 2. ☐ Certified copies of the priority documents have been received in Application No. _____.
 3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO/SB08)
Paper No(s)/Mail Date 5/01/2007
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date _____
- 5) ☐ Notice of Informal Patent Application
- 6) ☐ Other: _____

DETAILED ACTION

Election/Restrictions

1. Applicant's election with traverse of Group 1, Claims 1-9, 11, and 16-19 in the reply filed on 9/09/2008 is acknowledged. The traversal is on the ground(s) that the special technical feature is not the detection of IGF2 gene in cattle, but the detection of a specific polymorphism in the IGF2 gene in cattle (p. 6 1st full paragraph). This is not found persuasive because the claims are directing towards detecting a polymorphism present in the IGF2 gene at position 150 of SEQ ID NO. 1, Amarger et al. (as cited in the requirement for restriction) teaches the detection of the IGF2 gene in cattle (abstract) and therefore would detect the whole sequence and thereby detect "a polymorphism" in the IGF2 gene. The instant specification does not define the polymorphism therefore it is broadly interpreted as any nucleotide in that position.

The requirement is still deemed proper and is therefore made FINAL.

2. Claims 1-19 are pending. Claims 10 and 12-15 are withdrawn as being drawn to a nonelected invention.
3. An action of the merits for Claims 1-9, 11, and 16-19 is set forth below.

Information Disclosure Statement

4. The information disclosure statement (IDS) submitted on 5/01/2007 has been considered by the examiner.

The listing of the references in the specification is not a proper information disclosure statement (see p. 4-7 of the instant specification). 37 CFR 1.98(b) requires a list of all patents, publications or other information submitted for consideration by the Office, and MPEP §609.04(a) states "the list may not be incorporated into the specification but must be submitted in a separate paper." As such the references on p. 4-7 have not been considered unless they have been cited on form PTO-892 or the IDS submitted on 5/01/2007.

Claim Objections

5. Claims 1-9, 11, and 16-19 are objected to because of the following informalities: IGF2 is an abbreviation which should be spelled out. In claim 11 line 4 "CT" should be amended to "C/T". Appropriate correction is required.

Claim Rejections - 35 USC § 112/Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

6. Claims 1-9, 11, and 16-19 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1-9 are indefinite because the claims do not recite a clear nexus between the preamble of the claims and the process steps of the claims. The preamble states a method for identifying phenotypes in cattle. However the active process steps is

towards detecting a polymorphism. Therefore there is no positive active steps directed towards identifying phenotypes. It is therefore unclear how the identifying phenotypes is determined by detecting a polymorphism. Further the claim comprises a wherein clause which is not necessary for the actual positive active steps of the claims and therefore it is unclear what exactly is required to be detected.

Claims 2-7 are indefinite over the phrase "the presence or absence of at least one C allele" in lines 6-7 of claim 2. It is unclear if the "C allele" is the same as in claim 1 or if it encompasses another position in IGF2 not represented by position 150 of SEQ ID No. 1.

Claims 4-5 are rejected as being indefinite. Claim 4 recites the limitation "the polymorphism" in line 1. There is insufficient antecedent basis for this limitation in the claim. It is unclear if the phrase "the polymorphism" is referring to "a polymorphism present in the IGF2 gene at position 150" (line 2 Claim 1) or to "amplified IGF2 gene polymorphisms sequences" (line 4-5 Claim 2). It is suggested that the claim be amended to e.g. clearly point to the polymorphism with which it refers.

Claim 8 recites the limitation "the nucleic acid amplification products" in line 2. There is insufficient antecedent basis for this limitation in the claim. Claim 1 does not contain any limitation to nucleic acid amplification products. It is suggested that the claim be amended to e.g. clearly point to the nucleic acid amplification products with which it refers. Further Claim 8 is drawn to contacting "the nucleic acid amplification products" in line two, however, only hybridizes "the amplification product" in line 6. Therefore it is unclear if "the amplification product" in line 6 is one of the multiple

amplification products in line two or another amplification product which is not encompassed by the "nucleic acid amplification products" in line 2.

Claim 9 recites the limitation "the nucleic acid amplification product" in line 1. There is insufficient antecedent basis for this limitation in the claim. Claim 1 does not contain any limitation to nucleic acid amplification products. It is suggested that the claim be amended to e.g. clearly point to the nucleic acid amplification products with which it refers.

Claims 11 is indefinite because the claims do not recite a clear nexus between the preamble of the claims and the process steps of the claims. The preamble states a method for selecting individual cattle based on the knowledge of an animal's IGF2 genotype. However the active process steps is towards determining the IGF2 alleles of an animal and sorting animals into groups of like genotype. It is therefore unclear how determining the IGF2 alleles of an animal and sorting animals will select any individual cattle as the positive active steps do not include a step to select. Further the claim comprises a wherein clause which is not necessary for the actual positive active steps of the claims and therefore it is unclear what exactly is required to be detected.

Claim 11 is indefinite over the recitation of the phrase "with respect to" in line 4. It is unclear if the claim is towards alleles of a particular polymorphisms at a particular position or some other polymorphism at another position in some way related to position 150. It is suggested that the claim be amended to e.g. "C/C, C/T, or T/T detected at position 150 of SEQ ID No." to clearly indicate that the alleles are detected at position 150.

Claim 11 is indefinite because it is unclear if IGF2 alleles are determined in "an animal" or if "cattle" are used for the determination. Both the preamble and the wherein clause indicates a comparison of cattle, however, the method steps are towards detection of an animal.

Claims 16-17 are indefinite because the claims do not recite a clear nexus between the preamble of the claims and the process steps of the claims. The preamble states a method for identifying sires that will pass on a phenotype of lower birth weight to offspring. However the active process steps is towards detecting a polymorphism. Therefore there is no positive active steps directed towards identifying sires. It is therefore unclear how the identifying sires is determine by detecting a polymorphism. Further the claim comprises a wherein clause which is not necessary for the actual positive active steps of the claims and therefore it is unclear what exactly is required to be detected.

Claims 16-17 are indefinite over the phrase "will pass on a phenotype of lower birth weight to offspring" in lines 1-2 of Claim 16. It is unclear how the sire passes a phenotype because genotypes are passed to the offspring not the phenotype.

Claims 18 is indefinite because the claims do not recite a clear nexus between the preamble of the claims and the process steps of the claims. The preamble states a method of cattle production that reduces birth weight. However the active process steps is towards breeding dams to sires having a C residue. Therefore there is no positive active steps directed towards cattle production that reduces birth weight. It is therefore

unclear how the positive step of breeding with a particular genotype produces a reduced birth weight.

Claims 19 is indefinite because the claims do not recite a clear nexus between the preamble of the claims and the process steps of the claims. The preamble states a method of cattle production that increases birth weight. However the active process steps is towards breeding dams to sires having a T residue. Therefore there is no positive active steps directed towards cattle production that increase birth weight. It is therefore unclear how the positive step of breeding with a particular genotype produces a increased birth weight.

The term "reduces" in claim 18 and "increases" in claim 19 are relative terms which renders the claim indefinite. The terms "reduces" and "increases" are not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention. It is unclear how the birth weight is reduced or increased because there is no degree of reduction or increase with which it is compared.

Claim Rejections - 35 USC § 112/Scope of Enablement

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 1-9, 11, and 16-19 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for

A method for identifying increased rib eye area (REA) in bovine cattle, the method comprising isolating a genomic sample from bovine cattle, detecting a "C" or a "T" at position 150 of SEQ ID No. 1, identifying the bovine cattle with two copies of a "C" allele at position 150 of SEQ ID No. 1 as having increased REA compared to both bovine cattle with two copies of the "T" allele at position 150 of SEQ ID NO. 1 and bovine cattle with one copy of the "C" allele at position 150 of SEQ ID No. 1 and one copy of the "T" allele at position 150 of SEQ ID NO. 1.

A method for identifying decreased rib eye area (REA) in bovine cattle, the method comprising isolating a genomic sample from a bovine cattle, detecting a "C" or a "T" at position 150 of SEQ ID No. 1, identifying the bovine cattle with one copy of the "C" allele at position 150 of SEQ ID No. 1 and one copy of the "T" allele at position 150 of SEQ ID NO. 1 as having decreased REA compared to bovine cattle with two copies of the "C" allele at position 150 of SEQ ID No. 1.

A method for identifying sires that will pass on a genetic trait associated to lower birth weight in offspring, the method comprising isolating a genomic sample from a sire bovine cattle, detecting a "C" or a "T" at position 150 of SEQ ID No. 1, identifying the sire bovine cattle with two copies of a "C" allele at position 150 of SEQ ID No. 1 as having a genetic trait associated to lower birth weight in offspring as compared to a sire bovine cattle with two copies of a "T" allele at position 150 of SEQ ID No. 1.

A method for bovine cattle production that produces offspring with increased likelihood of reduced birth weight comprising breeding dam bovine cattle to sire bovine cattle in which two copies of a "C" allele has been detected at position 150 of SEQ ID No. 1 to produce progeny with increased likelihood of reduced birth weight as compared to offspring produced by a sire bovine cattle in which two copies of a "T" allele has been detected at position 150 of SEQ ID No. 1.

A method for bovine cattle production that produces offspring with increased likelihood of increased birth weight comprising breeding dam bovine cattle to sire bovine cattle in which two

copies of a "T" allele has been detected at position 150 of SEQ ID No. 1 to produced progeny with increased likelihood of increased birth weight as compared to offspring produced by a sire bovine cattle in which two copies of a "C" allele has been detected at position 150 of SEQ ID No. 1

, does not reasonably provide enablement for identifying any phenotype in any type of cattle, detecting any polymorphism at position 150 of SEQ ID No. 1, or associating a particular SNP with fat content or marbling (claims 1-9). The specification does not reasonable provide enablement for identifying any cattle, detecting an association with any IGF2 allele in any animal, and associations with fat content or marbling (claim 11). The specification does not provide reasonable enablement for detection of any polymorphism at Seq ID no. 1 in any cattle associated with birth weight (Claims 16-17). The specification does not provide reasonable enablement for producing any cattle that reduces or increases both weight. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make or use the invention commensurate in scope with these claims.

Factors to be considered in determining whether a disclosure meets the enablement requirement of 35 USC 112, first paragraph, have been described by the court in *In re Wands*, 8 USPQ2d 1400 (CA FC 1988). *Wands* states at page 1404,

"Factors to be considered in determining whether a disclosure would require undue experimentation have been summarized by the board in *Ex parte Forman*. They include (1) the quantity of experimentation necessary, (2) the amount of direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims."

Breadth of the claims

Claim 1 is drawn to a method for identifying phenotypes in cattle, comprising detecting a polymorphism present in the IGF2 gene at position 150 of SEQ ID No.1 and wherein the presence of a C residue is associated with phenotypes of at least one of increased rib eye area, decreased fat content, and decreased marbling as compared to cattle with a T residue at position 150 of SEQ ID No. 1. Claim 2 is drawn to isolation of DNA sample from the cattle to analyze the amplification products. Claim 3 defines the oligonucleotide pair. Claims 4-5 define the polymorphism. Claims 6-8 further include using a detectable moiety. Claim 9 defines the amplification method. Claim 11 is drawn to a method of selecting individual cattle based on the knowledge of an animal's IGF2 genotype comprising determining the IGF2 alleles of an animal, wherein the alleles of an animal are one of C/C, C/T, or T/T with respect to position 150 of SEQ ID No. 1 and sorting animals into groups of like genotype; and wherein a C/C or C/T genotype is associated with the phenotypes of increased rib eye area, decreased fat content, and marbling as compared to T/T cattle. Claim 16 is drawn to a method for identifying sires that will pass on a phenotype of lower birth weight to offspring comprising detecting a polymorphism in a sire present in the IGF2 gene at position 150 of SEQ ID No. 1 wherein the presence of a C residue at position 150 of SEQ ID No. 1 in both the IGF2 alleles is associated with the phenotype of production of offspring with lower birth weight as compared to sires with a T residue at position 150 of SEQ ID No. 1 in both IGF2 gene alleles. Claim 17 is drawn to isolating genomic DNA sample from cattle to analyze the presence or absence of a C allele and a T allele. Claim 18 is drawn to a method of cattle production that reduces either weight comprising breeding dams to alleles having

a C residue at position 150 of SEQ ID No. 1 in both IGF2 alleles. Claim 19 is drawn to a method of cattle production that increases birth weight comprising breeding dams to sires having a T residue at position 150 of SEQ ID No. 1 in both IGF2 gene alleles.

Claims 1-9 encompass identification of any phenotype in any cattle by detection of any polymorphism at position 150 and its association with REA, fat, or marbling. Claim 11 encompasses in any cattle the correlation of the detection of any IGF2 alleles with REA, fat, or marbling. Claims 16-17 encompass detection in any sire of any polymorphism at position 150 of SECT ID No. 1 and a correlation to any increased or decreased birth weight. Claims 18-19 encompass cattle production which reduces or increased any birth weight. Further these claims (18 and 19) are drawn to any sires have the C or T alleles at position 150 of SEQ ID NO. 1.

When the claims are read in light of the specification, the specification discloses a methodology but does not provide guidance for the broad interpretation of the claims. Further, though some of the claimed associations have significantly significant associations in the instant specification, as discussed below, some of the claimed associations have not been found significantly significant.

Nature of the Invention

The claims encompass detection in any cattle and an association of any polymorphism of IGF2 with any phenotype, and specifically, REA, fat, marbling, or birth weight.

The invention is in a class of invention which the CAFC has characterized as "the

unpredictable arts such as chemistry and biology.” Mycogen Plant Sci., Inc. v. Monsanto Co., 243 F.3d 1316, 1330 (Fed. Cir. 2001).

Teachings in the Specification

The specification discloses that insulin-like growth factor 2 (IGF2) is a 67 amino acid peptide hormone having multiple phenotypic effects on cellular growth and metabolism (p. 3 lines 13-15). The specification discloses that the IGF2 comprises 10 exons in pig and 9 exons in sheep (p. 3 lines 15-19). The specification discloses that there is no equivalent exon 2 in sheep (p. 3 lines 15-19). The specification asserts that the SNP of interest is in exon 2 of IGF2 and comprises a C to T transition at position 150 of SEQ ID No. 1 (p. 9 lines 1-5). The claims however are drawn to detecting any polymorphisms at position 150 of SEQ ID No. 1 (Claims 1-9, 16-17) or any alleles in IGF2 (Claim 11). Therefore the claims encompass detection of any nucleotide at position 150 of SEQ ID No. 1 or any nucleotide in IGF2. This would include mutations, variations, and insertions in IGF2. Although the instant specification provides examples of the detection of the C to T transition at position 150 of SNP of interest in exon 2 of IGF2, it does not provide support for the association of any phenotype, increased or decrease fat, marbling, or REA, or increased or decreased birth weight correlated with any polymorphisms at position 150 of SEQ ID no. 1 or any alleles in IGF2.

The instant specification defines “animal” to include all vertebrate animals including humans (p. 16 lines 18-19). The specification discloses that Cattle is generally to refer to an animal of bovine, however, the instant specification does not

specifically define cattle as only encompassing an animal of bovine (p. 17 lines 1-5). However, the art provides a definition of Cattle. Further the art teaches that cattle is defined as a neat cattle or an animal of the bovine species by whatever technical or familiar name it is known, and includes any horse, mule, ass, pig, sheep or goat (www.canlii.org/ca/sta/c-46/sec2.html). As disclosed by the instant specification, each species which is encompassed by the term cattle has a different genetic structure of IGF2. The specification discloses that the IGF2 comprises 10 exons in pig and 9 exons in sheep (p. 3 lines 15-19). The specification discloses that there is no equivalent exon 2 in sheep (p. 3 lines 15-19). Therefore the skilled artisan would have to perform a large amount of experimentation in order to ascertain equivalent polymorphism in the relevant species. Because the structures in these species are different, the associations made in one species can not be directly extrapolated to another species without further experimentation. Further, it is disclosed that sheep do not possess exon 2 therefore it is unpredictable that phenotypes can be associated with a SNP position located in exon 2 because the specification has not provided guidance as to the equivalent structure in the sheep IGF2 gene.

Claims 1-9 are drawn to identification of "any phenotype", the instant specification has not specifically defined this term. Phenotype of cattle encompasses any physical trait of cattle including color, hair type, and milk production amount to name a few types. However, the instant specification has only provided guidance to REA, fat, marbling, and birth weight. It is well known by the skilled artisan that each phenotype is controlled by different genes (and in some cases multiple genes) and that

a correlation of a association between one particular phenotype and genotype is not predictive of associations with any other phenotypes. Further the instant specification teaches that for some phenotypes (e.g. carcass weight) there is no significant correlation between the claimed SNP and a particular phenotype (p. 35 lines 1-5).

Working Examples

The instant specification discloses that 17 full-sib families of Canadian Beef cattle were used (p. 31 lines 5-9). The instant specification discloses a method of detection the SNP at position 150 of SEQ ID No. 1 as a C or a T to determine if the particular bovine is homozygous or heterozygous for the particular allele (p. 31- 33). The instant specification asserts detection in calves ranging from 1 to 560 days of age (p. 33 lines 6-10).

The specification asserts that in animals (e.g. Canadian beef cattle) the C/T allelic genotype had significantly smaller REA size compared to homozygous C/C offspring ($p=0.0004$) (p. 34 lines 10-15). The specification asserts that in the 125 cattle studies REA was significantly correlated with the number of C alleles present ($p=0.0001$) (p. 34 lines 10-17). The specification asserts that in 167 bulls REA was still positively correlated with the number of C alleles ($p=0.459$) and that cattle with C/C genotype had a significantly larger REA than the C/T or T/T genotype ($p=0.0413$) (p. 34 lines 20-23 and p. 35 lines 1-5). Therefore the instant specification provides a statistically significant correlation or increased or decreased REA wherein a bovine cattle has a specific genotype. However, this specific correlation between a particular

phenotypic trait and a genotype cannot be extrapolated to any phenotype and any genotype in any cattle species because each correlation is species and gene specific. An association of one phenotype to one genotype does not provide guidance to associations of any phenotype to any genotype.

The specification asserts that the specified SNP has an association with fat ($p = 0.0624$) and marbling ($p=0.0633$) (p. 35 lines 5-15). These are not statistically significant associations, and as such it would be unpredictable to association the detection of the C or T allele at position 150 of SNP 1 with increase or decrease fat or marbling content based upon guidance in the specification.

The specification asserts that birth weight is only affected by the allele inherited from the sire because of genetic imprinting of IGF2 (p. 35 lines 19-20). The specification asserts that offspring with the paternal C allele had a lower birth weight than offspring than those with a paternal T allele ($p=0.0132$) (p. 35 lines 20-24 and p. 36 lines 1-5). The specification discloses that no such effect was observed when the maternal allele was considered ($p=0.3234$) (p. 36 lines 1-5). The specification asserts that sires with C/C genotype will pass on the C allele to the offspring and therefore these calves will have lower birth weight (p. 36 lines 11-20). Therefore the specification provides a statistically significant p value for association a paternal C allele to lower birth weight of offspring, but the claim is directed towards reducing or increases birth weight. Therefore the claim encompasses the physical transformation of producing a cattle and then reducing the birth weight or increasing the birth weight. The association presented in the specification, however, is towards producing offspring that have

reduced birth weight when a sire is used with a CC genotype compared to offspring produced with by a sire with a TT genotype or producing offspring that have increased birth weight when a sire is used with a TT genotype compared to offspring produced with by a sire with a CC genotype.

The predictability or unpredictability of the art and degree of experimentation

Nezer et al. (Nature genetics Feb 1999 Vol 21 p. 155) teaches a correlation of 21 distinct phenotypes in pig offspring with the IGF2 gene (p. 155 1st paragraph). Nezer et al. teaches the detection of the exon 2 region of IGF2 (p. 155 2nd column). Nezer et al. teaches the correlation to phenotypes of fat deposition, belly fat, leaf fat, and jowl fat (p. 155 2nd paragraph) however, each of these phenotypes have a different associations to the IGF2 gene which indicates that different types of fat content of cattle is correlative to different genetic associations. Further Nezer et al. teaches the sequence of human IGF2 and pig IGF2 contains different exon structure (Figure 2) and therefore discloses that SNPs present in one animal is not directly correlative to any other species and as such a large amount of experimentation must be performed to determine equivalent SNP areas in each animal species.

Though the instant specification discloses a statistically predictable association of the SNP position and increased or decreased birth weight, there are many factors which affect the birth weight of a calf. Burris et al. (Journal of Animal Sciences 1952 Vol 11 p. 34) teaches that longer gestation period, age of the dam, and sex of the calf will influence birth weight (p. 36 last paragraph, p. 39 2nd paragraph, p. 39 last paragraph). Therefore the art teaches that there is many factors influencing birth weight and as such

the detection of the SNP is not the only influencing factor of weight.

Quantity of Experimentation

The quantity of experimentation in this area is extremely large since there is significant number of parameters which would have to be studied prior to being able to practice the claimed invention as broadly as written. The skilled artisan would have to determine an association of the polymorphism with any phenotype in any cattle. The skilled artisan would have to determine an association with any polymorphism at position 150 of SEQ ID NO. 1 and any IGF2 allele of any animal (Claim 11) with any phenotype, REA, fat, marbling, birth weight. This would require significant effort because the specification teaches that cattle have different structures with regard to IGF2 and that for some species, such as sheep, the structure does not have an equivalent exon 2 region (p. 3 lines 13-19). The specification further teaches that not all phenotypes are associated with the detection of a C or a T at position 150 of SEQ ID No. 1 (e.g. carcass weight is not associative). Further Nezer et al. teaches that the correlation of phenotypes with mutations of IGF2 is unpredictable wherein each of the phenotypes have a different association to the IGF2 gene. Therefore the claims as broadly encompassed would require significant inventive effort, with each of the many intervening steps, upon effective reduction to practice, not providing any guarantee of success in the succeeding steps.

Level of Skill in the Art

The level of skill in the art is deemed to be high.

Conclusion

Case law has established that '(t)o be enabling, the specification of a patent

must teach those skilled in the art how to make and use the full scope of the claimed invention without 'undue experimentation.'" *In re Wright* 990 F.2d 1557, 1561. *In re Fisher*, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970) it was determined that '(t)he scope of the claims must bear a reasonable correlation to the scope of enablement provided by the specification to persons of ordinary skill in the art". The amount of guidance needed to enable the invention is related to the amount of knowledge in the art as well as the predictability in the art. Furthermore, the Court in *Genetech Inc. v Novo Nordisk* 42 USPQ2d 1001 held that '(I)t is the specification, not the knowledge of one skilled in the art that must supply the novel aspects of the invention in order to constitute adequate enablement".

In the instant case, the specification has not provided a predictable association of identification of any phenotype in any cattle with any polymorphisms at position 150 of SEQ ID No. 1. The specification provides a statistically significant association with REA in bovine cattle and birth weight associations with sire genotypes, the specification indicates that there is no statistically significant association with fat or marbling. The specification discloses that the IGF2 gene is structurally different in various cattle species and that a SNP position in one cattle species is not correlative to another species. Further Nezer et al. teaches that phenotypes have different genetic associations with IGF2, as indicated by the different associations with various fat phenotypes tested in pig.

In view of this unpredictability, the specification has not established that the presently claimed method can be used to determine any phenotype in any cattle by

detecting any polymorphism at position 150 of SEQ ID No. 1.

Accordingly, in view of the unpredictability in the art, and the lack of disclosure in the specification and in the prior art and the unpredictability of the art, it would require undue experimentation for one of skill in the art to make and use the claimed invention.

Claim Rejections - 35 USC § 112/Written Description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

8. Claims 1-9, 11, 16-19 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 1 is drawn to a method for identifying phenotypes in cattle, comprising detecting a polymorphism present in the IGF2 gene at position 150 of SEQ ID No.1 and wherein the presence of a C residue is associated with phenotypes of at least one of increased rib eye area, decreased fat content, and decreased marbling as compared to cattle with a T residue at position 150 of SEQ ID No. 1. Claim 2 is drawn to isolation of DNA sample from the cattle to analyze the amplification products. Claim 3 defines the oligonucleotide pair. Claims 4-5 define the polymorphism. Claims 6-8 further include using a detectable moiety. Claim 9 defines the amplification method. Claim 11 is drawn

to a method of selecting individual cattle based on the knowledge of an animal's IGF2 genotype comprising determining the IGF2 alleles of an animal, wherein the alleles of an animal are one of C/C, C/T, or T/T with respect to position 150 of SEQ ID No. 1 and sorting animals into groups of like genotype; and wherein a C/C or C/T genotype is associated with the phenotypes of increased rib eye area, decreased fat content, and marbling as compared to T/T cattle. Claim 16 is drawn to a method for identifying sires that will pass on a phenotype of lower birth weight to offspring comprising detecting a polymorphism in a sire present in the IGF2 gene at position 150 of SEQ ID No. 1 wherein the presence of a C residue at position 150 of SEQ ID No. 1 in both the IGF2 alleles is associated with the phenotype of production of offspring with lower birth weight as compared to sires with a T residue at position 150 of SEQ ID No. 1 in both IGF2 gene alleles. Claim 17 is drawn to isolating genomic DNA sample from cattle to analyze the presence or absence of a C allele and a T allele. Claim 18 is drawn to a method of cattle production that reduces either weight comprising breeding dams to alleles having a C residue at position 150 of SEQ ID No. 1 in both IGF2 alleles. Claim 19 is drawn to a method of cattle production that increases birth weight comprising breeding dams to sires having a T residue at position 150 of SEQ ID No. 1 in both IGF2 gene alleles.

The claims are broadly drawn to any phenotype (Claims 1-9). The claims are broadly drawn to detection of any polymorphisms of SEQ ID No. 1 at position 150. Claim 11 is further drawn to detection of any IGF2 alleles. The claims are broadly drawn to any cattle.

The specification has not provided guidance as to which phenotypes are associated with the detection of the polymorphism at position 150 of SEQ ID No.1. The instant specification has not specifically defined "phenotype". Phenotype of cattle encompasses any physical trait of cattle including color, hair type, and milk production amount to name a few types. However, the instant specification has only provided guidance to REA, fat, marbling, and birth weight. It is well known by the skilled artisan that each phenotype is controlled by different genes (and in some cases multiple genes) and that a correlation of a association between one particular phenotype and genotype is not predictive of associations with any other phenotypes. The specification provides no predictable association between the specific polymorphism listed in the specification and the broad scope of phenotypes encompassed by the claims as the specification. Further the instant specification teaches that for some phenotypes (e.g. carcass weight) there is no significant correlation between the claimed SNP and a particular phenotype (p. 35 lines 1-5).

The claims encompass the term "cattle" which encompasses a broad genus of animals. The specification discloses that Cattle is generally to refer to an animal of bovine, however, the instant specification does not specifically define cattle as only encompassing an animal of bovine (p. 17 lines 1-5). However, the art provides a definition of Cattle. Further the art teaches that cattle is defined as a neat cattle or an animal of the bovine species by whatever technical or familiar name it is known, and includes any horse, mule, ass, pig, sheep or goat (www.canlii.org/ca/sta/c-46/sec2.html). As disclosed by the instant specification, each species which is

encompassed by the term cattle has a different genetic structure of IGF2. The specification discloses that the IGF2 comprises 10 exons in pig and 9 exons in sheep (p. 3 lines 15-19). The specification discloses that there is no equivalent exon 2 in sheep (p. 3 lines 15-19). Therefore the specification has not disclosed that the claimed SNP would be associated in any cattle. The specification provides no predictable association between the SNP in the specification and the broad scope of cattle as encompassed by the claims.

The specification discloses that insulin-like growth factor 2 (IGF2) is a 67 amino acid peptide hormone having multiple phenotypic effects on cellular growth and metabolism (p. 3 lines 13-15). The specification discloses that the IGF2 comprises 10 exons in pig and 9 exons in sheep (p. 3 lines 15-19). The specification discloses that there is no equivalent exon 2 in sheep (p. 3 lines 15-19). The specification asserts that the SNP of interest is in exon 2 of IGF2 and comprises a C to T transition at position 150 of SEQ ID No. 1 (p. 9 lines 1-5).

Therefore, the instant claims broadly encompass a genus of any nucleotide at position 150 of SEQ ID No. 1 and any allele of IGF2 (claim 11). However the specification has not provided clear description for the critical structure of these encompassed nucleotides with the functionality of detecting phenotypes or birth weight. The specification provides specific associations of a C or a T allele at position 150 of SEQ ID No. 1 and its association with specific phenotypes (p. 35-36). The genus includes an enormous number of polymorphisms and alleles for which no written description is provided in the specification. This large genus is represented in the

specification by only the particularly named SNP of a C to a T allele at position 150 of SEQ ID NO. 1 and a subset of phenotypes. Here, no common element or attributes of the sequences are disclosed which would permit selection of sequences as polymorphisms or mutations. No structural limitations or requirements which provide guidance on the identification of sequences which meet these functional limitations of associating a polymorphism or allele of IGF2 with any phenotype or birth weight is provided.

Accordingly, the specification lacks written description of any species representative of the broadly claimed genus.

In analysis of the claims for compliance with the written description requirement of 35 U.S.C. 112, first paragraph, the written description guidelines note regarding genus/species situations that "Satisfactory disclosure of a ``representative number" depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed." (See: "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 2001.) In the instant case, the specification fails to teach the necessary common attributes or features of the genus of encompassed nucleic acids and polymorphisms in view of the species disclosed. As such, one of skill in the art would not recognize that applicant was in possession of the genus of nucleic acids, the genus of phenotypes, and the genus of cattle as encompassed by the broadly claimed invention.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

5. Claims 1, 11, and 16 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The claims are drawn to method for identifying phenotypes in cattle (claim 1); a method of selecting individual cattle based on the knowledge of an animal's IGF2 genotype (claim 11); and a method of identifying sires that will pass on a phenotype of lower birth weight (claim 16).

The method of Claim 1 as claimed does not produce any physical transformation nor is the method tied to a machine. The claim as written encompass mere mental steps i.e. detecting a polymorphism. The method steps encompass identifying a SNP which can be accomplished by looking at a published database of nucleotides. A claimed process meets the criteria of 35 USC 101 if it is tied to a particular machine or apparatus or if it transforms a particular article into a different state or thing. Herein in the instant case the claim as witting does not require a particular machine or apparatus nor is there a transformation step. Further it is noted that Claim 2 which depends from Claim 1 encompasses a step of physical transformation (e.g. isolating a genomic DNA sample) therefore the further dependent claim indicates that the scope of Claim 1

encompasses methods without a step of physical transformation.

The method of Claim 11 as claimed does not produce any physical transformation nor is the method tied to a machine. The claim as written encompasses mere mental steps i.e. determining the IGF2 alleles and sorting animals into groups of like genotype. The method steps encompass determining the IGF2 alleles which can be accomplished by looking at a published database of nucleotides and sorting animals into groups which can be accomplished by visually sorting the data observed. A claimed process meets the criteria of 35 USC 101 if it is tied to a particular machine or apparatus or if it transforms a particular article into a different state or thing. Herein in the instant case the claim as written does not require a particular machine or apparatus nor is there a transformation step.

The method of Claim 16 as claimed does not produce any physical transformation nor is the method tied to a machine. The claim as written encompasses mere mental steps i.e. detecting a polymorphism. The method steps encompass identifying a SNP which can be accomplished by looking at a published database of nucleotides. A claimed process meets the criteria of 35 USC 101 if it is tied to a particular machine or apparatus or if it transforms a particular article into a different state or thing. Herein in the instant case the claim as written does not require a particular machine or apparatus nor is there a transformation step. Further it is noted that Claim 17 which depends from Claim 16 encompasses a step of physical transformation (e.g. isolating a genomic DNA sample) therefore the further dependent claim indicates that the scope of Claim 16 encompasses methods without a step of

physical transformation.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

9. Claims 18-19 are rejected under 35 U.S.C. 102(b) as being anticipated by Engellandt et al. (Journal of Animal Breeding and Genetics 2002 Vol. 119 p. 154).

With regard to Claims 18-19, the preambles, “cattle production that reduces birth weight” and “cattle production that increases birth weight” is not given any patentable weight. The preamble is an intended use and does not impart any further structural limitations.

Engellandt et al. teaches breeding dams to sires to produce a cattle population (p. 156 2nd column). Engellandt et al. teaches that the IGF2 gene is present in the population (abstract). It is inherent in a given population of sires that at least one sire would have the wild type genotype at position 150 of SEQ ID No. 1 (e.g. the C residue in the IGF2). Further, the instant specification discloses that in a population of 124 animals that 108 animals had a paternal C alleles wherein 14 animals had a paternal T allele therefore it is inherent in a general population that the allelic frequency of the C alleles is around 87% and the allelic frequency of the T allele is around 11%. Therefore it is inherent in a population of 210 sires (p. 156 2nd paragraph) that at least one of these

sires has a C/C genotype and at least one has a T/T genotype.

Conclusion

10. No Claims are allowed.

11. Any inquiry concerning this communication or earlier communications from the examiner should be directed to KATHERINE SALMON whose telephone number is (571)272-3316. The examiner can normally be reached on Monday-Friday 8AM-430PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached on (571) 272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Katherine Salmon/
Examiner, Art Unit 1634

/Juliet C Switzer/
Primary Examiner, Art Unit 1634